Reversible Somatic Dynamics — Phase-space diagram & math overview

This document contains a compact **mathematical model**, **phase-space diagram**, and **bifurcation sketch** that formalize the idea of reversing plasmid-driven somatic changes and locating the "somanal asymptote" (the boundary of reversibility). Use this as a single-page reference or share/print it.

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1. High-level model

- State space: $X \subseteq \mathbb{R}^n$ — a continuous representation of a somatic cell's internal state. Example coordinates: gene-expression levels, average epigenetic marks, plasmid copy number, DNA damage score.
- State vector: $x(t) \in X$, where $x = (g_1, \ldots, g_k, e_1, \ldots, e_m, p)$. Here p = plasmid-related variable (copy number / integration index).

Dynamics are driven by a controlled (or uncontrolled) flow:

$$\dot{x} = F(x; \theta, u(t))$$

- θ = fixed biological parameters (repair rate, epigenetic restoration rate, mutation rate, degradation).
- $u(t)$ = external controller (treatment pulses, plasmid removal actions, CRISPRon/off toggles).

We will analyze two regimes: - **Reversible regime**: there exists a control policy $u(t)$ such that the flow is (practically) invertible back to a desirable region R_0 around the original state. - **Irreversible regime**: for some states, inversion is impossible or requires impractical control (e.g., due to fixed genetic mutations or crossing biophysical thresholds).

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2. Group vs semigroup formalism

- Let $\mathcal{S} = \{\Phi_t\}_{t \geq 0}$ be the set of forward-time maps generated by F (a semigroup under composition).
- If we can extend $\mathcal{S}$ to a group $\mathcal{G} = \{\Phi_t\}_{t \in \mathbb{R}}$ (i.e., $\Phi_{-t} = \Phi_t^{-1}$ exists for relevant t), then dynamics are reversible in that domain.
- Practically, reversibility holds only on a subset $X_{inv} \subseteq X$ where inverses exist (e.g., plasmid unintegrated, epigenetic marks not permanently altered).

Formally:

X_{inv} = \{x\in X:\exists\,\Phi_{-t}\text{ s.t. }\Phi_{-t}(\Phi_t(x))=x\text{ for all }t\in[0,T]\}\.

The **somanal asymptote** can be defined as the boundary ∂X_{inv} separating reversible from irreversible states.

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3. Simple 2D exemplar toy model (for the diagram)

Choose two coordinates: - g : a scalar representing a composite gene-expression program (0 = normal, 1 = modified/pathologic). - p : plasmid load/integration index (0 = none, 1 = fully integrated/mutated).

Dynamics:

$$\left\{\dot{g} = -a(g - g_0) + b\,p - c\,g^3\ \dot{p} = -\lambda p + u(t) - \mu H(g - g^*)\backslash \mathrm{n}\right.$$

- $a > 0$ = homeostatic pull toward basal expression g_0 .
- b = plasmid-driven expression perturbation.
- Nonlinearity $-cg^3$ creates multiple equilibria (bistability) modeling "cell-fate".
- λ = plasmid clearance rate; $u(t)$ = control (e.g., plasmid-clearing intervention).
- $\mu H(g - g^*)$ = irreversible integration term when g crosses threshold g^* (Heaviside H models an absorbing transition).

Key qualitative behaviors: - If g stays below g^* , plasmid load can be cleared and the system returns to the reversible basin. - If g crosses g^* , an absorbing term reduces p dynamics to include a permanent component; reversal may be impossible — this models a biological "point of no return".

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4. Phase-space diagram (schematic)

Below is a mermaid-style sketch and an ASCII fallback of the 2D phase plane showing basins, attractors, and the reversibility boundary.

```
flowchart TB
  subgraph Plane [Phase plane: (g,p)]
    A((Stable attractor: Normal))
    B((Stable attractor: Modified))
    C[Boundary: Partial irreversibility \n (\u03C0 = absorbing region)]
  end
  A ---|flow lines| C
  B ---|flow lines| C
  C --> B
  style A fill:#ddf,stroke:#333,stroke-width:1px
  style B fill:#fdd,stroke:#333,stroke-width:1px
  style C fill:#f9f,stroke:#333,stroke-width:2px,stroke-dasharray: 5 5
```

ASCII sketch:

```
 p  ^
    |        Modified attractor (B)
    |       *
```

```
    |      *  *
    |     *     *   <--- irreversible region (absorbing)  ---->
    |    *       *
    |   *         *
    |  *           *
    | *             *
    |*               *
    +---------------------------------> g
        Normal attractor (A)
```

Legend: - Normal attractor (A): basin where controllers can steer the system back to baseline. - Modified attractor (B): altered cell-fate; may or may not be reversible depending on p and whether the trajectory crosses the absorbing boundary. - Irreversibility boundary (∂X_{inv}): shown as a dashed/pink band — crossing this moves the state into a region where group inverses no longer exist.

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5. Bifurcation / asymptote analysis

Treat a control parameter α (e.g., cumulative plasmid exposure):

$$\dot{g} = f(g, p; \alpha), \quad \dot{p} = g(g, p; \alpha)$$

As α increases, the system may undergo a saddle-node or transcritical bifurcation where the normal attractor disappears. The bifurcation point α_c is the **somanal asymptote** of reversibility: beyond α_c typical control inputs cannot restore the original state.

Sketch of bifurcation diagram (qualitative):

```
g*  |       ____ Modified branch (stable)
    |      /
    |_____/
    |    \   Normal branch (stable)  <-- disappears at alpha_c
    |     \
    +---------------------> alpha
         alpha_c
```

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6. Metrics to quantify reversibility & distance to asymptote

1. **Lyapunov distance to basin boundary**: compute minimal perturbation along trajectories that sends the state across ∂X_{inv} .
2. **Control energy to invert**: minimum L^2 or L^∞ norm of control $u(t)$ required to drive $x(T)$ back into R_0 .
3. **Time-to-recover**: minimal time T^* such that $\Phi_{-T^*}(x(T)) \in R_0$ under optimal control.

These define operational thresholds useful to experimentalists: if control energy or time exceed plausible/ethical limits, the state is practically irreversible.

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7. How geneticists can use this framework

- Map experimental observables to coordinates in X and estimate model parameters θ from data (system identification).
- Simulate trajectories under treatment strategies $u(t)$ to estimate the basin of attraction R_0 and boundary ∂X_{inv} .
- Use optimal control theory (Pontryagin maximum principle, dynamic programming) to compute minimal interventions to return cells to reversible regions.
- Use bifurcation analysis to find safety margins (how much exposure before hitting α_c).

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8. Suggested simulation snippet (Python, conceptual)

```
# sketch: simulate the 2D toy model and plot phase plane
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

def F(state, t, a,b,c,lam,mu,g0,gstar):
    g,p = state
    dg = -a*(g-g0) + b*p - c*g**3
    dp = -lam*p - mu*(1.0 if g>gstar else 0.0)
    return [dg,dp]

# integrate for different initial conditions and plot vector field &
trajectories
```

(Use this to numerically find attractors and test reversibility under different $u(t)$ controllers.)

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9. Next steps / customization

If you'd like, I can: - Create a polished vector diagram (SVG) of the phase plane and bifurcation plot. - Generate runnable code (with parameter values) and a set of example simulations. - Extend the model to higher dimension (e.g., include an explicit epigenetic variable and stochastic noise terms).

End of canvas document.